



SEQUENCE LISTING

<110> BARCHFELD, Gail
DEL GIUDICE, Giuseppe
RAPPUOLI, Rino

<120> DETOXIFIED MUTANTS OF BACTERIAL ADP RIBOSYLATING TOXINS
AS PARENTERAL ADJUVANTS

<130> 2302 1393 / PP01393.002

<140> 09/044,696

<141> 1998 03 18

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

<211> 711

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(708)

<220>

<223> Description of Artificial Sequence: wild-type Subunit
A from E. coli heat labile toxin

<400> 1

aat ggc gac aga tta tac cgt gct gac tct aga ccc cca gat gaa ata	48
Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile	
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aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga	96
Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg	
20 25 30	
gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa	144
Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln	
35 40 45	
acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt	192
Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser	
50 55 60	
ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca	240
Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser	
65 70 75 80	
ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta	288
Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val	
85 90 95	
att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta	336

50	55	60
Leu Arg Ser Ala His	Leu Ala Gly Gln Tyr	Ile Leu Ser Gly Tyr Ser
65	70	75 80
Leu Thr Ile Tyr	Ile Val Ile Ala Asn Met	Phe Asn Val Asn Asp Val
	85	90 95
Ile Ser Val Tyr	Ser Pro His Pro Tyr Glu	Gln Glu Val Ser Ala Leu
	100	105 110
Gly Gly Ile Pro Tyr	Ser Gln Ile Tyr Gly Trp	Tyr Arg Val Asn Phe
	115	120 125
Gly Val Ile Asp Glu	Arg Leu His Arg Asn Arg	Glu Tyr Arg Asp Arg
	130	135 140
Tyr Tyr Arg Asn Leu	Asn Ile Ala Pro Ala Glu	Asp Gly Tyr Arg Leu
	145	150 155 160
Ala Gly Phe Pro	Pro Asp His Gln Ala Trp	Arg Glu Glu Pro Trp Ile
	165	170 175
His His Ala Pro	Gln Gly Cys Gly Asp Ser	Ser Arg Thr Ile Thr Gly
	180	185 190
Asp Thr Cys Asn Glu	Glu Thr Gln Asn Leu Ser	Thr Ile Tyr Leu Arg
	195	200 205
Glu Tyr Gln Ser Lys	Val Lys Arg Gln Ile Phe	Ser Asp Tyr Gln Ser
	210	215 220
Glu Val Asp Ile Tyr	Asn Arg Ile Arg Asp	Glu Leu
	225	230 235

<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(720)

<220>
 <223> Description of Artificial Sequence: wild-type CT
 subunit A

<400> 3	
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Asn Asp Asp Lys Leu Tyr Arg	Ala Asp Ser Arg Pro Pro Asp Glu Ile
1	5 10 15
aag cag tca ggt ggt ctt atg	cca aga gga cag agt gag tac ttt gac 96
Lys Gln Ser Gly Gly Leu Met	Pro Arg Gly Gln Ser Glu Tyr Phe Asp

	20	25	30	
cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act				144
Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr				
	35	40	45	
cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att				192
Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile				
	50	55	60	
agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat				240
Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His				
	65	70	75	80
tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac				288
Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn				
	85	90	95	
gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa				336
Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu				
	100	105	110	
gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat				384
Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr				
	115	120	125	
cga gtt cat ttt ggg gtg ctt gat gaa caa tta cat cgt aat agg ggc				432
Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly				
	130	135	140	
tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat				480
Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp				
	145	150	155	160
ggg tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa				528
Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu				
	165	170	175	
gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga				576
Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg				
	180	185	190	
tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta				624
Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val				
	195	200	205	
aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca				672
Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser				
	210	215	220	
ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta				720
Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu				
	225	230	235	240
tga				723

<210> 4
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: wild-type CT
 subunit A

<400> 4
 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
 1 5 10 15
 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
 20 25 30
 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
 35 40 45
 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
 50 55 60
 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
 65 70 75 80
 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
 85 90 95
 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
 100 105 110
 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
 115 120 125
 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
 130 135 140
 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
 145 150 155 160
 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
 165 170 175
 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
 180 185 190
 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
 195 200 205
 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
 210 215 220
 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
 225 230 235 240